

09/446415

420 Rec'd PCT/PTO 20 DEC 1999.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Beamer, Lesa J., Carroll, Stephen F., Eisenber, David
- (ii) TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein: Crystallization, X-Ray Diffraction, Three-Dimensional Structure Determination, Rational Drug Design and Molecular Modeling of Related Proteins
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: McAndrews, Held & Malloy
 - (B) STREET: 500 West Madison, 34th Floor
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60661
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: McNicholas, Janet M.
 - (B) REGISTRATION NUMBER: 32,918
 - (C) REFERENCE/DOCKET NUMBER: 11034US01;100-248
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 312/707-8889
 - (B) TELEFAX: 312/707-9155
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 31..1491

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 124..1491

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rBPI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|--|-----|
| CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC | 54 |
| Met Arg Glu Asn Met Ala Arg Gly | |
| -31 -30 -25 | |
| CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA | 102 |
| Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile | |
| -20 -15 -10 | |
| GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC | 150 |
| Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile | |
| -5 1 5 | |
| TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG | 198 |
| Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu | |
| 10 15 20 25 | |
| CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT | 246 |
| Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe | |
| 30 35 40 | |
| AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC | 294 |
| Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp | |
| 45 50 55 | |
| ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT | 342 |
| Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn | |
| 60 65 70 | |
| GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGC | 390 |
| Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly | |
| 75 80 85 | |
| AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC | 438 |
| Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp | |
| 90 95 100 105 | |
| CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT | 486 |
| Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser | |
| 110 115 120 | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| AAC | CCC | ACG | TCA | GGC | AAG | CCC | ACC | ATC | ACC | TGC | TCC | AGC | TGC | AGC | AGC | 534 |
| Asn | Pro | Thr | Ser | Gly | Lys | Pro | Thr | Ile | Thr | Cys | Ser | Ser | Cys | Ser | Ser | |
| | | | 125 | | | | | 130 | | | | | 135 | | | |
| CAC | ATC | AAC | AGT | GTC | CAC | GTG | CAC | ATC | TCA | AAG | AGC | AAA | GTC | GGG | TGG | 582 |
| His | Ile | Asn | Ser | Val | His | Val | His | Ile | Ser | Lys | Ser | Lys | Val | Gly | Trp | |
| | | 140 | | | | | 145 | | | | | 150 | | | | |
| CTG | ATC | CAA | CTC | TTC | CAC | AAA | AAA | ATT | GAG | TCT | GCG | CTT | CGA | AAC | AAG | 630 |
| Leu | Ile | Gln | Leu | Phe | His | Lys | Lys | Ile | Glu | Ser | Ala | Leu | Arg | Asn | Lys | |
| | 155 | | | | | 160 | | | | | 165 | | | | | |
| ATG | AAC | AGC | CAG | GTC | TGC | GAG | AAA | GTG | ACC | AAT | TCT | GTA | TCC | TCC | AAG | 678 |
| Met | Asn | Ser | Gln | Val | Cys | Glu | Lys | Val | Thr | Asn | Ser | Val | Ser | Ser | Lys | |
| 170 | | | | | 175 | | | | | 180 | | | | | 185 | |
| CTG | CAA | CCT | TAT | TTC | CAG | ACT | CTG | CCA | GTA | ATG | ACC | AAA | ATA | GAT | TCT | 726 |
| Leu | Gln | Pro | Tyr | Phe | Gln | Thr | Leu | Pro | Val | Met | Thr | Lys | Ile | Asp | Ser | |
| | | | | 190 | | | | | 195 | | | | | 200 | | |
| GTG | GCT | GGA | ATC | AAC | TAT | GGT | CTG | GTG | GCA | CCT | CCA | GCA | ACC | ACG | GCT | 774 |
| Val | Ala | Gly | Ile | Asn | Tyr | Gly | Leu | Val | Ala | Pro | Pro | Ala | Thr | Thr | Ala | |
| | | | 205 | | | | | 210 | | | | | 215 | | | |
| GAG | ACC | CTG | GAT | GTA | CAG | ATG | AAG | GGG | GAG | TTT | TAC | AGT | GAG | AAC | CAC | 822 |
| Glu | Thr | Leu | Asp | Val | Gln | Met | Lys | Gly | Glu | Phe | Tyr | Ser | Glu | Asn | His | |
| | | 220 | | | | | 225 | | | | | 230 | | | | |
| CAC | AAT | CCA | CCT | CCC | TTT | GCT | CCA | CCA | GTG | ATG | GAG | TTT | CCC | GCT | GCC | 870 |
| His | Asn | Pro | Pro | Pro | Phe | Ala | Pro | Pro | Val | Met | Glu | Phe | Pro | Ala | Ala | |
| | 235 | | | | | 240 | | | | | 245 | | | | | |
| CAT | GAC | CGC | ATG | GTA | TAC | CTG | GGC | CTC | TCA | GAC | TAC | TTC | TTC | AAC | ACA | 918 |
| His | Asp | Arg | Met | Val | Tyr | Leu | Gly | Leu | Ser | Asp | Tyr | Phe | Phe | Asn | Thr | |
| 250 | | | | | 255 | | | | | 260 | | | | | 265 | |
| GCC | GGG | CTT | GTA | TAC | CAA | GAG | GCT | GGG | GTC | TTG | AAG | ATG | ACC | CTT | AGA | 966 |
| Ala | Gly | Leu | Val | Tyr | Gln | Glu | Ala | Gly | Val | Leu | Lys | Met | Thr | Leu | Arg | |
| | | | 270 | | | | | 275 | | | | | | 280 | | |
| GAT | GAC | ATG | ATT | CCA | AAG | GAG | TCC | AAA | TTT | CGA | CTG | ACA | ACC | AAG | TTC | 1014 |
| Asp | Asp | Met | Ile | Pro | Lys | Glu | Ser | Lys | Phe | Arg | Leu | Thr | Thr | Lys | Phe | |
| | | | 285 | | | | | 290 | | | | | 295 | | | |
| TTT | GGA | ACC | TTC | CTA | CCT | GAG | GTG | GCC | AAG | AAG | TTT | CCC | AAC | ATG | AAG | 1062 |
| Phe | Gly | Thr | Phe | Leu | Pro | Glu | Val | Ala | Lys | Lys | Phe | Pro | Asn | Met | Lys | |
| | 300 | | | | | | 305 | | | | | 310 | | | | |
| ATA | CAG | ATC | CAT | GTC | TCA | GCC | TCC | ACC | CCG | CCA | CAC | CTG | TCT | GTG | CAG | 1110 |
| Ile | Gln | Ile | His | Val | Ser | Ala | Ser | Thr | Pro | Pro | His | Leu | Ser | Val | Gln | |
| | 315 | | | | | 320 | | | | | 325 | | | | | |
| CCC | ACC | GGC | CTT | ACC | TTC | TAC | CCT | GCC | GTG | GAT | GTC | CAG | GCC | TTT | GCC | 1158 |
| Pro | Thr | Gly | Leu | Thr | Phe | Tyr | Pro | Ala | Val | Asp | Val | Gln | Ala | Phe | Ala | |
| 330 | | | | | 335 | | | | | 340 | | | | | 345 | |

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|---|------|
| GTC CTC CCC AAC TCC TCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His 350 355 360 | 1206 |
| ACA ACT GGT TCC ATG GAG GTC AGC GCC GAG TCC AAC AGG CTT GTT GGA Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly 365 370 375 | 1254 |
| GAG CTC AAG CTG GAT AGG CTG CTC CTG GAA CTG AAG CAC TCA AAT ATT Glu Leu Lys Leu Asp Arg Leu Leu Glu Leu Lys His Ser Asn Ile 380 385 390 | 1302 |
| GGC CCC TTC CCG GTT GAA TTG CTG CAG GAT ATC ATG AAC TAC ATT GTA Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val 395 400 405 | 1350 |
| CCC ATT CTT GTG CTG CCC AGG GTT AAC GAG AAA CTA CAG AAA GGC TTC Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe 410 415 420 425 | 1398 |
| CCT CTC CCG ACG CCG GCC AGA GTC CAG CTC TAC AAC GTA GTG CTT CAG Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln 430 435 440 | 1446 |
| CCT CAC CAG AAC TTC CTG CTG TTC GGT GCA GAC GTT GTC TAT AAA Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys 445 450 455 | 1491 |
| TGAAGGCACC AGGGGTGCCG GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGGC | 1551 |
| ACCGGCTGCC TTTCCCCAGG GAATCCTCTC CAGATCTTAA CCAAGAGCCC CTTGCAAACT | 1611 |
| TCTTCGACTC AGATTCAGAA ATGATCTAAA CACGAGGAAA CATTATTCAT TGGAAAAGTG | 1671 |
| CATGGTGTGT ATTTTAGGGA TTATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT | 1731 |
| CCTCCAGGAA TCGTGTTTCA ATTGTAACCA AGAAATTTCC ATTTGTGCTT CATGAAAAAA | 1791 |
| AACTTCTGGT TTTTTCATG TG | 1813 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| |
|--|
| Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val -31 -30 -25 -20 |
| Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val -15 -10 -5 1 |

Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
 5 10 15
 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
 20 25 30
 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
 35 40 45
 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
 50 55 60 65
 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
 70 75 80
 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
 85 90 95
 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
 100 105 110
 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
 115 120 125
 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
 130 135 140 145
 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
 150 155 160
 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
 165 170 175
 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
 180 185 190
 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
 195 200 205
 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
 210 215 220 225
 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
 230 235 240
 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
 245 250 255
 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
 260 265 270
 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
 275 280 285
 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
 290 295 300 305

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Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
 310 315 320
 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
 325 330 335
 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
 340 345 350
 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
 355 360 365
 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
 370 375 380 385
 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
 390 395 400
 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
 405 410 415
 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
 420 425 430
 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
 435 440 445
 Gly Ala Asp Val Val Tyr Lys
 450 455

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